OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 23:05:16 ; Search time 1868 Seconds
(without alignments)
427.917 Million cell updates/sec

Title: US-10-646-436-10
Perfect score: 21
Sequence: 1 gcagcagagucuucaucautt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.4	92.4	532	9	CE099065	CE099065 tigr-gss-
c	2	19.4	92.4	573	2	BF921577	BF921577 MR1-NT017
c	3	19	90.5	85	2	AW276802	AW276802 xp66a01.x
	4	19	90.5	100	2	BF920141	BF920141 MR1-NT017
c	5	19	90.5	102	4	BF958934	BF958934 PM1-NN120
c	6	19	90.5	119	2	AW901233	AW901233 CM4-NN101
c	7	19	90.5	124	4	BM821731	BM821731 K-EST0090
	8	19	90.5	136	6	CD612966	CD612966 56043322J
c	9	19	90.5	137	6	CD612965	CD612965 56043322H
c	10	19	90.5	138	5	BQ339862	BQ339862 PM1-NN120
c	11	19	90.5	142	7	D45267	D45267 HUMHG1194 H
	12	19	90.5	147	5	BQ339466	BQ339466 PM1-NN120
	13	19	90.5	148	2	BF846357	BF846357 PM1-EN006
c	14	19	90.5	149	7	R47195	R47195 CBS-389 Sub
c	15	19	90.5	169	2	BE766895	BE766895 RC2-NT011
c	16	19	90.5	177	1	AL048592	AL048592 DKFZp586H
	17	19	90.5	183	4	BI032792	BI032792 MR4-NN018
c	18	19	90.5	184	4	BF958930	BF958930 PM1-NN120
c	19	19	90.5	185	4	BI036860	BI036860 MR4-NT014
	20	19	90.5	196	1	AI745406	AI745406 wc37d01.x
c	21	19	90.5	197	4	BI036862	BI036862 MR4-NT014
c	22	19	90.5	201	4	BF957666	BF957666 PM1-NN120
c	23	19	90.5	203	4	BF957653	BF957653 PM1-NN120
c	24	19	90.5	207	4	BF957858	BF957858 PM1-NN120
	25	19	90.5	211	2	BF928116	BF928116 MR4-NT014
c	26	19	90.5	224	2	AW161224	AW161224 au70a10.y
	27	19	90.5	226	2	BF935119	BF935119 MR4-NT014
	28	19	90.5	236	4	BF948789	BF948789 MR3-NN021
c	29	19	90.5	238	2	BF923639	BF923639 MR4-NT014
c	30	19	90.5	239	4	BG898974	BG898974 HOA21-1-C
c	31	19	90.5	241	7	CR767137	CR767137 DKFZp469B
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	33	19	90.5	244	2	BE766870	BE766870 RC2-NT011
c	34	19	90.5	248	2	BF923643	BF923643 MR4-NT014
	35	19	90.5	249	4	BF945175	BF945175 PM1-NN120
	36	19	90.5	250	5	BQ345410	BQ345410 MR4-NT014
c	37	19	90.5	252	2	BF923633	BF923633 MR4-NT014
	38	19	90.5	252	4	BF963107	BF963107 PM1-NN120
c	39	19	90.5	253	2	BF887875	BF887875 QV2-TN017
	40	19	90.5	253	4	BI041998	BI041998 MR4-NT014
	41	19	90.5	256	4	BI041248	BI041248 MR4-NT014
	42	19	90.5	257	6	CD612964	CD612964 56037472J
	43	19	90.5	258	4	BF961150	BF961150 PM1-NN120
c	44	19	90.5	258	7	CR763018	CR763018 DKFZp469G
	45	19	90.5	262	4	BF947155	BF947155 MR3-NN021

ALIGNMENTS

RESULT 1
CE099065/c
LOCUS CE099065 532 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000371093708 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE099065
VERSION CE099065.1 GI:35165950
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 532)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .532
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"
ORIGIN

Query Match 92.4%; Score 19.4; DB 9; Length 532;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
              |||||||||:|: ||:||:||
Db         82 GCAGCAGAGTCTACATCATTT 62
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RESULT 2
BF921577/c
LOCUS       BF921577                573 bp    mRNA    linear   EST 19-JAN-2001
DEFINITION  MR1-NT0179-171100-004-h01 NT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF921577
VERSION     BF921577.1  GI:12317465
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-NT0179-
            171100-004-h01&t3=2000-11-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 13
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0179"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             92.4%;  Score 19.4;  DB 2;  Length 573;
  Best Local Similarity   71.4%;  Pred. No. 2.1e+02;
  Matches   15;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
              |||||||||:|::||:||: |
Db         64 GCAGCAGAGTCTTCATCATCT 44


RESULT 3
AW276802/c
LOCUS       AW276802                 85 bp    mRNA    linear   EST 03-JAN-2000
DEFINITION  xp66a01.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745288 3'
            similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AW276802
VERSION     AW276802.1  GI:6663832
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
            Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2745288"
                     /sex="female"
                     /tissue_type="papillary serous ovarian metastasis"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ov39"
                     /note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT
                     priming.  Non-directionally cloned into the UDG sites of
                     pAMP10.  Size-selected on agarose gel, average insert
                     size 500 bp.  Primary library; non-amplified.  cDNA
                     Library Preparation: David B. Krizman, Ph.D (NCI).
                     Reference:  Krizman et al. (1996) Cancer Research
                     56:5380-5383."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 2;  Length 85;
  Best Local Similarity   73.7%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         80 GCAGCAGAGTCTTCATCAT 62


RESULT 4
BF920141
LOCUS       BF920141                100 bp    mRNA    linear   EST 19-JAN-2001
DEFINITION  MR1-NT0179-071100-003-f02 NT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF920141
VERSION     BF920141.1  GI:12316029
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
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            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-NT0179-
            071100-003-f02&t3=2000-11-07&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 100.
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0179"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 2;  Length 100;
  Best Local Similarity   73.7%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         58 GCAGCAGAGTCTTCATCAT 76


RESULT 5
BF958934/c
LOCUS       BF958934                102 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  PM1-NN1200-011200-009-b07 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF958934
VERSION     BF958934.1  GI:12376209
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 102)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-
            011200-009-b07&t3=2000-12-01&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 101.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NN1200"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 4;  Length 102;
  Best Local Similarity   73.7%;  Pred. No. 2.4e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         89 GCAGCAGAGTCTTCATCAT 71


RESULT 6
AW901233/c
LOCUS       AW901233                119 bp    mRNA    linear   EST 24-MAY-2000
DEFINITION  CM4-NN1011-100300-110-g04 NN1011 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW901233
VERSION     AW901233.1  GI:8065542
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 119)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM4-NN1011-100
            300-110-g04&t3=2000-03-10&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 118.
FEATURES             Location/Qualifiers
     source          1. .119
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
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                     /clone_lib="NN1011"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 2;  Length 119;
  Best Local Similarity   73.7%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        101 GCAGCAGAGTCTTCATCAT 83


RESULT 7
BM821731/c
LOCUS       BM821731                124 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0090952 S20T665307 Homo sapiens cDNA clone S20T665307-15-H01
            5', mRNA sequence.
ACCESSION   BM821731
VERSION     BM821731.1  GI:19178144
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 124)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 15  row: H  column: 01
            High quality sequence stop: 124.
FEATURES             Location/Qualifiers
     source          1. .124
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S20T665307-15-H01"
                     /sex="M"
                     /lab_host="Top10F'"
                     /clone_lib="S20T665307"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 4;  Length 124;
  Best Local Similarity   73.7%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        100 GCAGCAGAGTCTTCATCAT 82


RESULT 8
CD612966
LOCUS       CD612966                136 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56043322J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD612966
VERSION     CD612966.1  GI:40261230
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 136)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 136;
  Best Local Similarity   73.7%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         71 GCAGCAGAGTCTTCATCAT 89


RESULT 9
CD612965/c
LOCUS       CD612965                137 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56043322H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD612965
VERSION     CD612965.1  GI:40261229
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .137
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /db_xref="taxon:9606"
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                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             90.5%;  Score 19;  DB 6;  Length 137;
  Best Local Similarity   73.7%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         66 GCAGCAGAGTCTTCATCAT 48


RESULT 10
BQ339862/c
LOCUS       BQ339862                138 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  PM1-NN1200-011200-010-f07 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ339862
VERSION     BQ339862.1  GI:20999978
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 138)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-
            011200-010-f07&t3=2000-12-01&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NN1200"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 5;  Length 138;
  Best Local Similarity   73.7%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        125 GCAGCAGAGTCTTCATCAT 107


RESULT 11
D45267/c
LOCUS       D45267                  142 bp    mRNA    linear   EST 30-DEC-1995
DEFINITION  HUMHG1194 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.
ACCESSION   D45267
VERSION     D45267.1  GI:1136645
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 142)
  AUTHORS   Takahashi,N., Hashida,H., Zhao,N., Misumi,Y. and Sakaki,Y.
  TITLE     High-density cDNA filter analysis of the expression profiles of the
            genes preferentially expressed in human brain
  JOURNAL   Gene 164, 219-227 (1995)
  MEDLINE   96069586
   PUBMED   7590334
COMMENT     Contact: Nobuaki Takahashi
            Institute of Medical Science
            University of Tokyo
            Shirokanedi 4-6-1, Minato-ku, Tokyo, Japan 108
            Tel: 03-5449-5625
            Fax: 03-5449-5445.
FEATURES             Location/Qualifiers
     source          1. .142
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Human cerebral cortex"
                     /note="Adult male cerebral cortex tissue."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 7;  Length 142;
  Best Local Similarity   73.7%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         77 GCAGCAGAGTCTTCATCAT 59


RESULT 12
BQ339466
LOCUS       BQ339466                147 bp    mRNA    linear   EST 20-MAY-2002
DEFINITION  PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ339466
VERSION     BQ339466.1  GI:20999152
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 147)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
```

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1200-051100-004-h12&t3=2000-11-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 34.

FEATURES Location/Qualifiers
source 1. .147
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1200"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.5%; Score 19; DB 5; Length 147;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
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Db 124 GCAGCAGAGTCTTCATCAT 142

RESULT 13
BF846357
LOCUS BF846357 148 bp mRNA linear EST 16-JAN-2001
DEFINITION PM1-EN0065-231000-002-b01 EN0065 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF846357
VERSION BF846357.1 GI:12233611
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 148)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-EN0065-231000-002-b01&t3=2000-10-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 110.

FEATURES Location/Qualifiers
source 1. .148
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="EN0065"
/note="Organ: lung_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.5%; Score 19; DB 2; Length 148;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 36 GCAGCAGAGTCTTCATCAT 54

RESULT 14
R47195/c
LOCUS R47195 149 bp mRNA linear EST 12-DEC-1995
DEFINITION CBS-389 Subtractive cDNA library ocular ciliary body Homo sapiens cDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession number M64722), mRNA sequence.
ACCESSION R47195
VERSION R47195.1 GI:807537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 149)
AUTHORS Escribano,J., Ortego,J. and Coca-Prados,M.
TITLE Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: Transcription and synthesis of plasma proteins
JOURNAL J. Biochem. 118 (5), 921-931 (1995)
MEDLINE 96318503
PUBMED 8749308
COMMENT Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
Email: miguel_coca-prados@quickmail.yale.edu
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .149
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CBS-389"
/clone_lib="Subtractive cDNA library ocular ciliary body"
/note="Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; A subtractive cDNA library was developed by hybridizing antisense, single-stranded phagemid DNA (ssDNA) (as pBluescript SK-) from the ocular ciliary body cDNA library (target) of a 34-year-old female donor in lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular cell line cDNA library (driver) in the same vector."

ORIGIN

Query Match 90.5%; Score 19; DB 7; Length 149;
Best Local Similarity 73.7%; Pred. No. 2.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         69 GCAGCAGAGTCTTCATCAT 51


RESULT 15
BE766895/c
LOCUS       BE766895                169 bp    mRNA    linear   EST 19-SEP-2000
DEFINITION  RC2-NT0110-050600-013-f03 NT0110 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE766895
VERSION     BE766895.1  GI:10196819
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 169)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC2-NT0110-050
            600-013-f03&t3=2000-06-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 18
            High quality sequence stop: 169.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0110"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             90.5%;  Score 19;  DB 2;  Length 169;
  Best Local Similarity   73.7%;  Pred. No. 2.7e+02;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         57 GCAGCAGAGTCTTCATCAT 39


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	19	90.5	181	4	US-09-366-380-19	Sequence 19, Appl
c	3	19	90.5	181	5	PCT-US95-02303-18	Sequence 18, Appl
c	4	19	90.5	195	2	US-08-485-657A-14	Sequence 14, Appl
c	5	19	90.5	195	4	US-09-366-380-14	Sequence 14, Appl
c	6	19	90.5	195	5	PCT-US95-02303-14	Sequence 14, Appl
c	7	19	90.5	275	4	US-09-513-999C-11015	Sequence 11015, A
c	8	19	90.5	396	4	US-09-640-173-15	Sequence 15, Appl
c	9	19	90.5	396	4	US-09-713-550-15	Sequence 15, Appl
c	10	19	90.5	396	4	US-09-825-294-15	Sequence 15, Appl
c	11	19	90.5	396	4	US-09-970-966-15	Sequence 15, Appl
c	12	19	90.5	482	4	US-09-621-976-13267	Sequence 13267, A
c	13	19	90.5	491	4	US-09-513-999C-3749	Sequence 3749, Ap
	14	19	90.5	601	4	US-09-949-016-201815	Sequence 201815,
c	15	19	90.5	1648	3	US-09-659-791A-3	Sequence 3, Appli
c	16	19	90.5	1651	3	US-09-659-791A-13	Sequence 13, Appl
c	17	19	90.5	1825	4	US-09-949-016-5661	Sequence 5661, Ap
c	18	19	90.5	7610	3	US-09-659-791A-12	Sequence 12, Appl
c	19	19	90.5	17348	4	US-09-949-016-17403	Sequence 17403, A
c	20	18.4	87.6	448	4	US-09-513-999C-14310	Sequence 14310, A
c	21	16.8	80.0	334	3	US-09-227-357-90	Sequence 90, Appl
c	22	16.8	80.0	462	4	US-09-328-352-1618	Sequence 1618, Ap
	23	16.8	80.0	601	4	US-09-949-016-139518	Sequence 139518,
	24	16.8	80.0	75378	4	US-09-949-016-17140	Sequence 17140, A
c	25	16.8	80.0	117001	4	US-09-949-016-15684	Sequence 15684, A
	26	16.4	78.1	183112	4	US-09-949-016-14184	Sequence 14184, A
	27	16.2	77.1	32	4	US-09-410-935B-6	Sequence 6, Appli
	28	16.2	77.1	32	4	US-09-784-403A-6	Sequence 6, Appli
	29	16.2	77.1	222	4	US-09-270-767-30143	Sequence 30143, A
c	30	16.2	77.1	279	4	US-09-313-294A-2815	Sequence 2815, Ap
c	31	16.2	77.1	283	4	US-09-313-294A-1242	Sequence 1242, Ap
c	32	16.2	77.1	300	3	US-09-172-108-2	Sequence 2, Appli
c	33	16.2	77.1	300	3	US-09-172-711-3	Sequence 3, Appli
c	34	16.2	77.1	362	4	US-09-270-767-6149	Sequence 6149, Ap
c	35	16.2	77.1	362	4	US-09-270-767-21431	Sequence 21431, A
c	36	16.2	77.1	374	4	US-09-640-211A-1599	Sequence 1599, Ap
c	37	16.2	77.1	468	4	US-09-107-532A-2971	Sequence 2971, Ap
	38	16.2	77.1	547	4	US-09-702-705-89	Sequence 89, Appl
	39	16.2	77.1	547	4	US-09-736-457-89	Sequence 89, Appl
	40	16.2	77.1	547	4	US-09-614-124B-89	Sequence 89, Appl
	41	16.2	77.1	547	4	US-09-671-325-89	Sequence 89, Appl
	42	16.2	77.1	547	4	US-09-589-184-89	Sequence 89, Appl
	43	16.2	77.1	547	4	US-09-658-824-89	Sequence 89, Appl
c	44	16.2	77.1	550	3	US-08-998-416-148	Sequence 148, App
	45	16.2	77.1	601	4	US-09-949-016-173228	Sequence 173228,

ALIGNMENTS

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RESULT 1
US-08-485-657A-19/c
; Sequence 19, Application US/08485657A
; Patent No. 5942389
;  GENERAL INFORMATION:
;    APPLICANT:  Kirschling, Deborah J
;    APPLICANT:  Gudkov, Andrei
;    APPLICANT:  Roninson, Igor B
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive, 32nd Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,657A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5942389nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  93,354-N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  181 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-485-657A-19

  Query Match             90.5%;  Score 19;  DB 2;  Length 181;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
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Db         71 GCAGCAGAGTCTTCATCAT 53


RESULT 2
US-09-366-380-19/c
; Sequence 19, Application US/09366380
; Patent No. 6541603
;  GENERAL INFORMATION:
;    APPLICANT:  Kirschling, Deborah J
;    APPLICANT:  Gudkov, Andrei
;    APPLICANT:  Roninson, Igor B
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive, 32nd Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,380
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/199,900
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6541603nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  93,354-N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  181 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-380-19

  Query Match             90.5%;  Score 19;  DB 4;  Length 181;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         71 GCAGCAGAGTCTTCATCAT 53


RESULT 3
PCT-US95-02303-18/c
; Sequence 18, Application PC/TUS9502303
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  25
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02303
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  181 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-02303-18

  Query Match             90.5%;  Score 19;  DB 5;  Length 181;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         71 GCAGCAGAGTCTTCATCAT 53


RESULT 4
US-08-485-657A-14/c
; Sequence 14, Application US/08485657A
; Patent No. 5942389
;  GENERAL INFORMATION:
;    APPLICANT:  Kirschling, Deborah J
;    APPLICANT:  Gudkov, Andrei
;    APPLICANT:  Roninson, Igor B
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive, 32nd Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,657A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5942389nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  93,354-N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-485-657A-14

  Query Match             90.5%;  Score 19;  DB 2;  Length 195;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         85 GCAGCAGAGTCTTCATCAT 67


RESULT 5
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US-09-366-380-14/c
; Sequence 14, Application US/09366380
; Patent No. 6541603
;  GENERAL INFORMATION:
;    APPLICANT:  Kirschling, Deborah J
;    APPLICANT:  Gudkov, Andrei
;    APPLICANT:  Roninson, Igor B
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive, 32nd Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,380
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/199,900
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6541603nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  93,354-N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-380-14

  Query Match             90.5%;  Score 19;  DB 4;  Length 195;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         85 GCAGCAGAGTCTTCATCAT 67


RESULT 6
PCT-US95-02303-14/c
; Sequence 14, Application PC/TUS9502303
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Genes and Genetic Elements Associated
;    TITLE OF INVENTION:  with Sensitivity to Cisplatin
;    NUMBER OF SEQUENCES:  25
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02303
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  195 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-02303-14

  Query Match             90.5%;  Score 19;  DB 5;  Length 195;
  Best Local Similarity   73.7%;  Pred. No. 21;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         85 GCAGCAGAGTCTTCATCAT 67


RESULT 7
US-09-513-999C-11015/c
; Sequence 11015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 11015
;   LENGTH: 275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-11015

  Query Match             90.5%;  Score 19;  DB 4;  Length 275;
  Best Local Similarity   73.7%;  Pred. No. 22;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        126 GCAGCAGAGTCTTCATCAT 108


RESULT 8
US-09-640-173-15/c
; Sequence 15, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION:  OVARIAN TUMOR SEQUENCES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE:  210121.484C2
;  CURRENT APPLICATION NUMBER: US/09/640,173
;  CURRENT FILING DATE:  2000-08-15
;  NUMBER OF SEQ ID NOS:  196
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(396)
;   OTHER INFORMATION: n = A,T,C or G
US-09-640-173-15

  Query Match             90.5%;  Score 19;  DB 4;  Length 396;
  Best Local Similarity   73.7%;  Pred. No. 24;
```

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAGCAGAGUCUUCAUCAU 19
              ||||||||||:|::||:||:
Db         77 GCAGCAGAGTCTTCATCAT 59
```

RESULT 9
US-09-713-550-15/c
; Sequence 15, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-15

Query Match 90.5%; Score 19; DB 4; Length 396;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAGCAGAGUCUUCAUCAU 19
              ||||||||||:|::||:||:
Db         77 GCAGCAGAGTCTTCATCAT 59
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RESULT 10
US-09-825-294-15/c
; Sequence 15, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

Query Match 90.5%; Score 19; DB 4; Length 396;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAGCAGAGUCUUCAUCAU 19
              ||||||||||:|::||:||:
Db         77 GCAGCAGAGTCTTCATCAT 59
```

RESULT 11
US-09-970-966-15/c
; Sequence 15, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match 90.5%; Score 19; DB 4; Length 396;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAGCAGAGUCUUCAUCAU 19
              ||||||||||:|::||:||:
Db         77 GCAGCAGAGTCTTCATCAT 59
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RESULT 12
US-09-621-976-13267/c
; Sequence 13267, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13267
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13267

Query Match 90.5%; Score 19; DB 4; Length 482;
Best Local Similarity 73.7%; Pred. No. 24;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCAGCAGAGUCUUCAUCAU 19
              ||||||||||:|::||:||:
Db         94 GCAGCAGAGTCTTCATCAT 76
```

RESULT 13
US-09-513-999C-3749/c
; Sequence 3749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

```
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 3749
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 108..455
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 108..161
;   OTHER INFORMATION: score 6.3
;   OTHER INFORMATION: seq LLFVGLLLTWESG/QV
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 459
;   OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-3749

  Query Match             90.5%;  Score 19;  DB 4;  Length 491;
  Best Local Similarity   73.7%;  Pred. No. 24;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        126 GCAGCAGAGTCTTCATCAT 108


RESULT 14
US-09-949-016-201815
; Sequence 201815, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201815
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-201815

  Query Match             90.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   73.7%;  Pred. No. 25;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db        550 GCAGCAGAGTCTTCATCAT 568


RESULT 15
US-09-659-791A-3/c
; Sequence 3, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
;  FILE REFERENCE: RTS-0156
;  CURRENT APPLICATION NUMBER: US/09/659,791A
;  CURRENT FILING DATE:  2000-09-11
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
;   LENGTH: 1648
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (53)...(1402)
US-09-659-791A-3

  Query Match             90.5%;  Score 19;  DB 3;  Length 1648;
  Best Local Similarity   73.7%;  Pred. No. 29;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         71 GCAGCAGAGTCTTCATCAT 53


Search completed: May 24, 2005, 00:23:40
Job time : 106 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 21:40:56 ; Search time 255 Seconds
(without alignments)
487.508 Million cell updates/sec

Title: US-10-646-436-10
Perfect score: 21
Sequence: 1 gcagcagagucuucaucautt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		21	100.0	21	12	ADL70465	Adl70465 RNAi for
2		21	100.0	21	12	ADL70431	Adl70431 RNAi for
c 3		19	90.5	19	12	ADL70522	Adl70522 RNAi for
4		19	90.5	19	12	ADL70523	Adl70523 RNAi for
c 5		19	90.5	19	12	ADL70444	Adl70444 RNAi for
6		19	90.5	19	12	ADL70445	Adl70445 RNAi for
7		19	90.5	21	3	AAA94226	Aaa94226 Human tes
8		19	90.5	21	10	ACF36398	Acf36398 TRPM-2 an
9		19	90.5	21	11	ADM83069	Adm83069 Human TRP
c 10		19	90.5	21	12	ADL70464	Adl70464 RNAi for
c 11		19	90.5	21	12	ADL70430	Adl70430 RNAi for
12		19	90.5	21	12	ADL70406	Adl70406 Antisense
c 13		19	90.5	23	12	ADL70521	Adl70521 Human clu
c 14		19	90.5	195	2	AAT00416	Aat00416 Genetic s
c 15		19	90.5	275	3	AAC06940	Aac06940 Human sec
c 16		19	90.5	396	4	AAF94824	Aaf94824 Human ova
c 17		19	90.5	396	6	ABL48774	Abl48774 Ovarian c
c 18		19	90.5	396	6	ABT03091	Abt03091 Human ova
c 19		19	90.5	396	11	ADM10684	Adm10684 Human ova
c 20		19	90.5	396	12	ADJ11014	Adj11014 Represent
c 21		19	90.5	396	12	ADM43275	Adm43275 Human ova
c 22		19	90.5	461	9	ACH44960	Ach44960 Human foe
c 23		19	90.5	462	9	ACH15312	Ach15312 Human adu
c 24		19	90.5	465	9	ACH44965	Ach44965 Human foe
c 25		19	90.5	490	9	ACH25299	Ach25299 Human adu
c 26		19	90.5	491	3	AAC03751	Aac03751 Human sec
c 27		19	90.5	491	9	ACH30243	Ach30243 Human tes
c 28		19	90.5	492	9	ACH43944	Ach43944 Human foe
c 29		19	90.5	512	2	AAV89150	Aav89150 EST clone
c 30		19	90.5	572	2	AAZ42136	Aaz42136 Human nor
c 31		19	90.5	704	6	ABQ56105	Abq56105 Human ova
c 32		19	90.5	922	3	AAA43857	Aaa43857 Human sec
c 33		19	90.5	1024	10	ABZ83527	Abz83527 Toxicolog
c 34		19	90.5	1067	8	ACC90611	Acc90611 Human CGD
c 35		19	90.5	1117	8	ACC90613	Acc90613 Human CGD
c 36		19	90.5	1315	8	ACC90621	Acc90621 Human CGD
c 37		19	90.5	1369	8	ACC90610	Acc90610 Human CGD
c 38		19	90.5	1373	8	ACC90622	Acc90622 Human CGD
c 39		19	90.5	1451	10	ADI02673	Adi02673 Human cDN
c 40		19	90.5	1568	5	AAS44948	Aas44948 cDNA enco
c 41		19	90.5	1589	6	ABS78654	Abs78654 Human cDN
c 42		19	90.5	1610	8	ACC90609	Acc90609 Human CGD
c 43		19	90.5	1648	6	ABN99656	Abn99656 Human clu
c 44		19	90.5	1651	2	AAQ11503	Aaq11503 Cytolysis
c 45		19	90.5	1651	6	ABN99666	Abn99666 Human clu

ALIGNMENTS

RESULT 1
ADL70465
ID ADL70465 standard; RNA; 21 BP.
XX
AC ADL70465;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 20. .21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= dTdT"
XX
PN WO2004018676-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001277.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
DR WPI; 2004-226852/21.
XX
PT New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's

```
PT   disease or cancer.
XX
PS   Claim 4; SEQ ID NO 10; 63pp; English.
XX
CC   The present sequence is the antisense strand of a short interfering RNA
CC   (siRNA) targeted to human clusterin. The sense strand is also provided
CC   ADL70464. The siRNA can be used to interfere with the expression of
CC   clusterin. Clusterin, also known as testosterone-repressed prostate
CC   message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
CC   increased amounts by prostate tumour cells following androgen withdrawal,
CC   and has also been shown to be critical for neuritic toxicity in mouse
CC   models of Alzheimer's disease. siRNAs of the invention can be used alone
CC   or in combination with other chemotherapy or apoptosis inducing
CC   treatments for the treatment of prostate cancer, sarcomas such as
CC   osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
CC   cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
CC   melanoma, and also for the treatment of Alzheimer's disease.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

  Query Match             100.0%;  Score 21;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
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Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
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Db          1 GCAGCAGAGUCUUCAUCAUTT 21


RESULT 2
ADL70431
ID   ADL70431 standard; RNA; 21 BP.
XX
AC   ADL70431;
XX
DT   20-MAY-2004  (first entry)
XX
DE   RNAi for human clusterin.
XX
KW   Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW   short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /mod_base= OTHER
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XX
PN   WO2004018675-A1.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001276.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   02-DEC-2002; 2002US-0319748P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (GLEA/) GLEAVE M E.
XX
PI   Jansen B;
XX
DR   WPI; 2004-226851/21.
XX
PT   Treating melanoma in a mammalian subject comprises administering to the
PT   subject a therapeutic agent effective to reduce the effective amount of
PT   clusterin in the melanoma cells.
XX
PS   Claim 20; SEQ ID NO 29; 32pp; English.
XX
CC   The present sequence is that of a short interfering RNA (siRNA) molecule
CC   targeted to human clusterin ADL70403. The invention relates to the
CC   treatment of melanoma through reduction in the effective amount of
CC   clusterin. The therapeutic agent may be an antisense oligonucleotide
CC   ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC   targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC   mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC   line comprises administering an agent effective to modulate the amount of
CC   clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC   is down-regulated when the effective amount of clusterin is reduced. Such
CC   inhibition is significant because bcl-xL is known to act as an inhibitor
CC   of apoptosis.
XX
SQ   Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

  Query Match             100.0%;  Score 21;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
              |||||||||||||||||||||
Db          1 GCAGCAGAGUCUUCAUCAUTT 21


RESULT 3
ADL70522/c
ID   ADL70522 standard; RNA; 19 BP.
XX
AC   ADL70522;
XX
DT   20-MAY-2004  (first entry)
XX
DE   RNAi for human clusterin.
XX
KW   RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW   cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   18. .19
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= dTdT"
XX
PN   WO2004018676-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001277.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Jansen B,  Gleave ME,  Signaevsky M,  Beraldi E,  Trougakos IP;
PI   Gonos ES;
XX
DR   WPI; 2004-226852/21.
XX
PT   New RNA molecule less than 49 bases and having a sequence effective to
PT   mediate degradation or block translation of mRNA that is the
PT   transcriptional product of a target gene, useful for treating Alzheimer's
PT   disease or cancer.
XX
PS   Claim 4; SEQ ID NO 67; 63pp; English.
XX
```

CC The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC The antisense strand is also provided ADL70523. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
SQ Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

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  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         19 GCAGCAGAGTCTTCATCAT 1
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RESULT 4
ADL70523
ID ADL70523 standard; RNA; 19 BP.
XX
AC ADL70523;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 18. .19
FT /*tag= a
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FT /note= "OTHER= dTdT"
XX
PN WO2004018676-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001277.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
DR WPI; 2004-226852/21.
XX
PT New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
PS Claim 4; SEQ ID NO 68; 63pp; English.
XX
CC The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC The sense strand is also provided ADL70522. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
SQ Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

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  Query Match             90.5%;  Score 19;  DB 12;  Length 19;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||||||||||||
Db          1 GCAGCAGAGUCUUCAUCAU 19
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RESULT 5
ADL70444/c
ID ADL70444 standard; RNA; 19 BP.
XX
AC ADL70444;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
PN WO2004018675-A1.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
PI Jansen B;
XX
DR WPI; 2004-226851/21.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.

```
XX
PS   Claim 20; SEQ ID NO 42; 32pp; English.
XX
CC   The present sequence is that of a short interfering RNA (siRNA) molecule
CC   targeted to human clusterin ADL70403. The invention relates to the
CC   treatment of melanoma through reduction in the effective amount of
CC   clusterin. The therapeutic agent may be an antisense oligonucleotide
CC   ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC   targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC   mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC   line comprises administering an agent effective to modulate the amount of
CC   clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC   is down-regulated when the effective amount of clusterin is reduced. Such
CC   inhibition is significant because bcl-xL is known to act as an inhibitor
CC   of apoptosis.
XX
SQ   Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 33;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 6
ADL70445
ID   ADL70445 standard; RNA; 19 BP.
XX
AC   ADL70445;
XX
DT   20-MAY-2004  (first entry)
XX
DE   RNAi for human clusterin.
XX
KW   Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW   short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /mod_base= OTHER
FT                   /note= "OTHER= TT"
XX
PN   WO2004018675-A1.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001276.
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PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   02-DEC-2002; 2002US-0319748P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (GLEA/) GLEAVE M E.
XX
PI   Jansen B;
XX
DR   WPI; 2004-226851/21.
XX
PT   Treating melanoma in a mammalian subject comprises administering to the
PT   subject a therapeutic agent effective to reduce the effective amount of
PT   clusterin in the melanoma cells.
XX
PS   Claim 20; SEQ ID NO 43; 32pp; English.
XX
CC   The present sequence is that of a short interfering RNA (siRNA) molecule
CC   targeted to human clusterin ADL70403. The invention relates to the
CC   treatment of melanoma through reduction in the effective amount of
CC   clusterin. The therapeutic agent may be an antisense oligonucleotide
CC   ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC   targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC   mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC   line comprises administering an agent effective to modulate the amount of
CC   clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC   is down-regulated when the effective amount of clusterin is reduced. Such
CC   inhibition is significant because bcl-xL is known to act as an inhibitor
CC   of apoptosis.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||||||||||||
Db          1 GCAGCAGAGUCUUCAUCAU 19


RESULT 7
AAA94226
ID   AAA94226 standard; DNA; 21 BP.
XX
AC   AAA94226;
XX
DT   12-JAN-2001  (first entry)
XX
DE   Human testosterone-repressed prostate message-2 antisense oligo #2.
XX
KW   Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW   sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200049937-A2.
XX
PD   31-AUG-2000.
XX
PF   25-FEB-2000; 2000WO-US004875.
XX
PR   26-FEB-1999;   99US-0121726P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave M,  Rennie PS,  Miyake H,  Nelson C;
XX
DR   WPI; 2000-533132/48.
XX
PT   Treating prostatic tumors and renal cancers by antisense inhibition of
PT   the testosterone-repressed prostate messenger-2 gene.
XX
PS   Claim 3; Page 36; 38pp; English.
XX
CC   The present sequence is an antisense oligonucleotide directed at the
CC   human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC   clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC   promote the regression of tumours, and oligonucleotides directed at human
CC   TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC   gene. These include prostate cancer, renal cell cancer and some breast
CC   cancer cells. In addition to this, they also increase the
CC   chemosensitivity of the cells, meaning that conventional chemotherapy is
CC   more effective
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 3;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 8
ACF36398
ID   ACF36398 standard; DNA; 21 BP.
XX
AC   ACF36398;
XX
DT   18-DEC-2003  (first entry)
XX
DE   TRPM-2 antisense oligonucleotide.
XX
KW   TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW   prostate cancer; anti-apoptotic protein; antisense; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003072591-A1.
XX
PD   04-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005305.
XX
PR   22-FEB-2002; 2002US-00080794.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave M,  Rennie PS,  Miyake H,  Nelson C,  Monia BP;
XX
DR   WPI; 2003-689981/65.
XX
PT   New modified antisense oligonucleotide, useful particularly for treating
PT   prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
PS   Claim 1; Page 25; 44pp; English.
XX
CC   The invention relates to a compound consisting of an oligonucleotide with
CC   a phosphorothioate backbone throughout, in which: (a) sugars on
CC   nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC   remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC   positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC   ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC   prostatic cancer cells to the androgen-independent state, in vivo or in
CC   vitro; (b) to treat prostatic cancer (after initially withdrawing
CC   androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC   cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC   ovarian and some breast cancer cells) that express abnormal levels of
CC   TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC   increase stability in vivo and activity (both in vivo or in vitro) and
CC   result in a synergistic increase in effect when (I) is used with
CC   chemotherapeutic agents or other antisense oligonucleotides directed
CC   against other antiapoptotic genes. The present sequence represents a
CC   specific example of an anti-apoptotic protein TRPM-2 (testosterone-
CC   repressed prostate message-2) antisense oligonucleotide
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 10;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 9
ADM83069
ID   ADM83069 standard; DNA; 21 BP.
XX
AC   ADM83069;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human TRPM-2 antisense oligonucleotide #4.
XX
KW   Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW   radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW   lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "Phosphorothioate backbone"
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PN   US2003158130-A1.
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PD   21-AUG-2003.
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PF   28-SEP-2001; 2001US-00967726.
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PR   25-FEB-2000; 2000WO-US004875.
PR   28-SEP-2000; 2000US-0236301P.
PR   10-AUG-2001; 2001US-00913325.
XX
PA   (GLEA/) GLEAVE M.
PA   (RENN/) RENNIE P S.
PA   (MIYA/) MIYAKE H.
PA   (NELS/) NELSON C.
PA   (ZELL/) ZELLWEGER T.
XX
PI   Gleave M,  Rennie PS,  Miyake H,  Nelson C,  Zellweger T;
XX
DR   WPI; 2003-778017/73.
XX
PT   Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT   that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT   comprises administering a composition that inhibits expression of TRPM-2.
XX
PS   Claim 4; SEQ ID NO 4; 14pp; English.
XX
CC   The present invention provides a method for treating cancer in which
CC   cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC   The invention is useful for enhancing the chemo-sensitivity or radiation-
CC   sensitivity of cancer cells for treating cancer such as prostate cancer,
CC   bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC   (RCC). The invention is also useful in antisense gene therapy. The
CC   present sequence is human testosterone-repressed prostate message-2 (TRPM
CC   -2) antisense oligodeoxyribonucleotide (ODN).
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 11;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 10
ADL70464/c
ID   ADL70464 standard; RNA; 21 BP.
XX
AC   ADL70464;
```

```
XX
DT   20-MAY-2004  (first entry)
XX
DE   RNAi for human clusterin.
XX
KW   RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW   cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   20. .21
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= dTdT"
XX
PN   WO2004018676-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001277.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Jansen B,  Gleave ME,  Signaevsky M,  Beraldi E,  Trougakos IP;
PI   Gonos ES;
XX
DR   WPI; 2004-226852/21.
XX
PT   New RNA molecule less than 49 bases and having a sequence effective to
PT   mediate degradation or block translation of mRNA that is the
PT   transcriptional product of a target gene, useful for treating Alzheimer's
PT   disease or cancer.
XX
PS   Claim 4; SEQ ID NO 9; 63pp; English.
XX
CC   The present sequence is the sense strand of a short interfering RNA
CC   (siRNA) targeted to human clusterin. The antisense strand is also
CC   provided ADL70465. The siRNA can be used to interfere with the expression
CC   of clusterin. Clusterin, also known as testosterone-repressed prostate
CC   message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
CC   increased amounts by prostate tumour cells following androgen withdrawal,
CC   and has also been shown to be critical for neuritic toxicity in mouse
CC   models of Alzheimer's disease. siRNAs of the invention can be used alone
CC   or in combination with other chemotherapy or apoptosis inducing
CC   treatments for the treatment of prostate cancer, sarcomas such as
CC   osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
CC   cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
CC   melanoma, and also for the treatment of Alzheimer's disease.
XX
SQ   Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 11
ADL70430/c
ID   ADL70430 standard; RNA; 21 BP.
XX
AC   ADL70430;
XX
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```
DT   20-MAY-2004  (first entry)
XX
DE   RNAi for human clusterin.
XX
KW   Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW   short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   20. .21
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= TT"
XX
PN   WO2004018675-A1.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001276.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   02-DEC-2002; 2002US-0319748P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (GLEA/) GLEAVE M E.
XX
PI   Jansen B;
XX
DR   WPI; 2004-226851/21.
XX
PT   Treating melanoma in a mammalian subject comprises administering to the
PT   subject a therapeutic agent effective to reduce the effective amount of
PT   clusterin in the melanoma cells.
XX
PS   Claim 20; SEQ ID NO 28; 32pp; English.
XX
CC   The present sequence is that of a short interfering RNA (siRNA) molecule
CC   targeted to human clusterin ADL70403. The invention relates to the
CC   treatment of melanoma through reduction in the effective amount of
CC   clusterin. The therapeutic agent may be an antisense oligonucleotide
CC   ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC   targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC   mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC   line comprises administering an agent effective to modulate the amount of
CC   clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC   is down-regulated when the effective amount of clusterin is reduced. Such
CC   inhibition is significant because bcl-xL is known to act as an inhibitor
CC   of apoptosis.
XX
SQ   Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 12
ADL70406
ID   ADL70406 standard; DNA; 21 BP.
XX
AC   ADL70406;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Antisense oligonucleotide to human clusterin.
```

```
XX
KW   Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .21
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FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate nucleotides"
FT   modified_base   1. .4
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'O-methoxyethyl modifications"
FT   modified_base   18. .21
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'O-methoxyethyl modifications"
XX
PN   WO2004018675-A1.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001276.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   02-DEC-2002; 2002US-0319748P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (GLEA/) GLEAVE M E.
XX
PI   Jansen B;
XX
DR   WPI; 2004-226851/21.
XX
PT   Treating melanoma in a mammalian subject comprises administering to the
PT   subject a therapeutic agent effective to reduce the effective amount of
PT   clusterin in the melanoma cells.
XX
PS   Claim 7; SEQ ID NO 4; 32pp; English.
XX
CC   The present sequence is that of an antisense oligonucleotide targeted to
CC   human clusterin ADL70403. The invention relates to the treatment of
CC   melanoma through reduction in the effective amount of clusterin. The
CC   therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
CC   or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
CC   The antisense oligonucleotides are complementary to a region of the
CC   clusterin mRNA spanning either the translation initiation site or the
CC   termination site. They may be modified to increase stability in vivo,
CC   e.g. they may be employed as phosphorothioate derivatives and may have 2'
CC   -O-(2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The
CC   present antisense oligonucleotide is particularly preferred. It is
CC   targeted to the translation initiation codon and next 6 codons of the
CC   human clusterin sequence. It has a phosphorothioate backbone throughout
CC   and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an
CC   example from the invention, this antisense oligonucleotide provided a
CC   dose-dependent down-regulation of clusterin in human melanoma cells,
CC   leading to an increase in apoptotic cell death. In one melanoma cell line
CC   (607B) this alone was sufficient to lead to complete cell death. In
CC   another melanoma cell line, the surviving cells showed increased
CC   sensitivity to subsequent treatment with cisplatin. A claimed method for
CC   regulating expression of bcl-xL in a subject or cell line comprises
CC   administering an agent effective to modulate the amount of clusterin
CC   expression. In clusterin-expressing cells, expression of bcl-xL is down-
CC   regulated when the effective amount of clusterin is reduced. Such
CC   inhibition is significant because bcl-xL is known to act as an inhibitor
CC   of apoptosis.
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 13
ADL70521/c
ID   ADL70521 standard; cDNA; 23 BP.
XX
AC   ADL70521;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human clusterin target for RNAi.
XX
KW   RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW   cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004018676-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-CA001277.
XX
PR   21-AUG-2002; 2002US-0405193P.
PR   03-SEP-2002; 2002US-0408152P.
PR   20-MAY-2003; 2003US-0472387P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Jansen B,  Gleave ME,  Signaevsky M,  Beraldi E,  Trougakos IP;
PI   Gonos ES;
XX
DR   WPI; 2004-226852/21.
XX
PT   New RNA molecule less than 49 bases and having a sequence effective to
PT   mediate degradation or block translation of mRNA that is the
PT   transcriptional product of a target gene, useful for treating Alzheimer's
PT   disease or cancer.
XX
PS   Example 6; SEQ ID NO 66; 63pp; English.
XX
CC   The present sequence is a human clusterin cDNA target for a double-
CC   stranded short interfering RNA (siRNA) of the invention ADL70522-
CC   ADL70523. It was used in an example from the invention to demonstrate
CC   clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
CC   known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC   glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC   tumour cells following androgen withdrawal, and has also been shown to be
CC   critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC   siRNAs of the invention can be used alone or in combination with other
CC   chemotherapy or apoptosis inducing treatments for the treatment of
CC   prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC   breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC   anaplastic large cell lymphoma and melanoma, and also for the treatment
CC   of Alzheimer's disease.
XX
SQ   Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 12;  Length 23;
  Best Local Similarity   73.7%;  Pred. No. 34;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
```

```
Db         21 GCAGCAGAGTCTTCATCAT 3


RESULT 14
AAT00416/c
ID   AAT00416 standard; cDNA; 195 BP.
XX
AC   AAT00416;
XX
DT   26-MAR-1996  (first entry)
XX
DE   Genetic suppressor element HL7.1.
XX
KW   Genetic suppressor element; GSE; platinum-based drug; cisplatin;
KW   chemotherapy; HL7.1; testosterone-repressed prostatic message-2; TRPM-2;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9522612-A2.
XX
PD   24-AUG-1995.
XX
PF   22-FEB-1995;   95WO-US002303.
XX
PR   22-FEB-1994;   94US-00199900.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Kirschling DJ,  Gudkov A,  Roninson IB;
XX
DR   WPI; 1995-302718/39.
XX
PT   Genetic suppressor elements which confer resistance to platinum-based
PT   drugs, eg. cisplatin, on cancer cells - useful for enhancement of
PT   chemotherapy, and for diagnosis of resistance to these drugs.
XX
PS   Claim 14; Fig 17; 75pp; English.
XX
CC   The sequences represented by AAT00405-T00418 are genetic suppressor
CC   elements (GSEs). This sequence represents GSE HL6.10. This sequence shows
CC   homology to the cDNA encoding testosterone-repressed prostatic message-2
CC   (TRPM-2). These sequences were obtained from a cDNA library derived from
CC   the total cDNA of a cisplatin sensitive cell. Genetic suppressor elements
CC   confer resistance to platinum-based drugs (PDs), such as cisplatin. These
CC   functional GSEs can then be used to create probes for the parent gene.
CC   The probes can then be used in a method of measuring the level of GSE
CC   gene expression. The GSEs can be used in methods of diagnosis of
CC   resistance to PDs by measuring the level of expression of GSE genes. The
CC   GSEs are also used in methods to overcome resistance to PDs in cancer
CC   cells. The GSEs (or fragments of them) can be used to inhibit the
CC   function of genes associated with sensitivity to PDs. For enhancement of
CC   chemotherapy, a GSE can be transferred (either alone or with another
CC   gene) on an expression vector into blood progenitor cells from a cancer
CC   patient. The cells are returned to the patients circulation and allowed
CC   to repopulate the blood before aggressive chemotherapy is carried out
CC   (using higher cisplatin concentrations than normal), this will thereby
CC   avoid toxic side effects to the immune system as the blood cells will be
CC   GSE resistant
XX
SQ   Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 2;  Length 195;
  Best Local Similarity   73.7%;  Pred. No. 48;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         85 GCAGCAGAGTCTTCATCAT 67


RESULT 15
AAC06940/c
ID   AAC06940 standard; cDNA; 275 BP.
XX
AC   AAC06940;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 11015.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS   Claim 1; SEQ ID NO 11015; 71pp + Sequence Listing; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC   ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC   to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC   diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors
XX
SQ   Sequence 275 BP; 59 A; 88 C; 85 G; 43 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 19;  DB 3;  Length 275;
  Best Local Similarity   73.7%;  Pred. No. 51;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db        126 GCAGCAGAGTCTTCATCAT 108


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Job time : 259 secs
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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	6	CQ786122	CQ786122 Sequence
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c 3	19	90.5	19	6	CQ786179	CQ786179 Sequence
4	19	90.5	19	6	CQ786180	CQ786180 Sequence
c 5	19	90.5	19	6	CQ786653	CQ786653 Sequence
6	19	90.5	19	6	CQ786654	CQ786654 Sequence
c 7	19	90.5	21	6	CQ786121	CQ786121 Sequence
8	19	90.5	21	6	CQ786615	CQ786615 Sequence
c 9	19	90.5	21	6	CQ786639	CQ786639 Sequence
c 10	19	90.5	23	6	CQ786178	CQ786178 Sequence
c 11	19	90.5	181	6	AR302789	AR302789 Sequence
c 12	19	90.5	195	6	AR302784	AR302784 Sequence
c 13	19	90.5	255	6	CQ693037	CQ693037 Sequence
c 14	19	90.5	270	6	CQ688092	CQ688092 Sequence
c 15	19	90.5	275	6	AX895152	AX895152 Sequence
c 16	19	90.5	275	6	BD030685	BD030685 Sequence
c 17	19	90.5	306	6	CQ684015	CQ684015 Sequence
c 18	19	90.5	396	6	AR391192	AR391192 Sequence
c 19	19	90.5	396	6	AR392897	AR392897 Sequence
c 20	19	90.5	396	6	AR489627	AR489627 Sequence
c 21	19	90.5	396	6	AR493868	AR493868 Sequence
c 22	19	90.5	396	6	AX093197	AX093197 Sequence
c 23	19	90.5	482	6	AR421770	AR421770 Sequence
c 24	19	90.5	482	6	AX982464	AX982464 Sequence
c 25	19	90.5	482	6	BD117323	BD117323 EST and e
c 26	19	90.5	491	6	AX887886	AX887886 Sequence
c 27	19	90.5	491	6	BD027496	BD027496 Sequence
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ALIGNMENTS

RESULT 1
CQ786122
LOCUS CQ786122 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 10 from Patent WO2004018676.
ACCESSION CQ786122
VERSION CQ786122.1 GI:45721225
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 10 04-MAR-2004;
The University of British Columbia (CA)
FEATURES Location/Qualifiers
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 76.2%; Pred. No. 33;
Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAUTT 21
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Db 1 GCAGCAGAGTCTTCATCATTT 21

RESULT 2
CQ786640
LOCUS CQ786640 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 29 from Patent WO2004018675.
ACCESSION CQ786640
VERSION CQ786640.1 GI:45721660
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct

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           other sequences; artificial sequences.
REFERENCE  1
  AUTHORS  Jansen,B.
  TITLE    Treatment of melanoma by reduction in clusterin levels
  JOURNAL  Patent: WO 2004018675-A 29 04-MAR-2004;
           The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES             Location/Qualifiers
     source          1. .21
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                     /note="RNAi for human clusterin"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 6;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 33;
  Matches   16;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
              |||||||||:|::||:||:||
Db          1 GCAGCAGAGTCTTCATCATTT 21


RESULT 3
CQ786179/c
LOCUS       CQ786179                  19 bp    RNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 67 from Patent WO2004018676.
ACCESSION   CQ786179
VERSION     CQ786179.1  GI:45721282
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
  TITLE     Rnai probes targeting cancer-related proteins
  JOURNAL   Patent: WO 2004018676-A 67 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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                     /note="RNAi for human clusterin"
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Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 4
CQ786180
LOCUS       CQ786180                  19 bp    RNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 68 from Patent WO2004018676.
ACCESSION   CQ786180
VERSION     CQ786180.1  GI:45721283
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
  TITLE     Rnai probes targeting cancer-related proteins
  JOURNAL   Patent: WO 2004018676-A 68 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          1 GCAGCAGAGTCTTCATCAT 19


RESULT 5
CQ786653/c
LOCUS       CQ786653                  19 bp    RNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 42 from Patent WO2004018675.
ACCESSION   CQ786653
VERSION     CQ786653.1  GI:45721673
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B.
  TITLE     Treatment of melanoma by reduction in clusterin levels
  JOURNAL   Patent: WO 2004018675-A 42 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES             Location/Qualifiers
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 6
CQ786654
LOCUS       CQ786654                  19 bp    RNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 43 from Patent WO2004018675.
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VERSION     CQ786654.1  GI:45721674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B.
  TITLE     Treatment of melanoma by reduction in clusterin levels
  JOURNAL   Patent: WO 2004018675-A 43 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES             Location/Qualifiers
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Db          1 GCAGCAGAGTCTTCATCAT 19


RESULT 7
CQ786121/c
LOCUS       CQ786121                  21 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 9 from Patent WO2004018676.
ACCESSION   CQ786121
VERSION     CQ786121.1  GI:45721224
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
  TITLE     Rnai probes targeting cancer-related proteins
  JOURNAL   Patent: WO 2004018676-A 9 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 8
CQ786615
LOCUS       CQ786615                  21 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 4 from Patent WO2004018675.
ACCESSION   CQ786615
VERSION     CQ786615.1  GI:45721635
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jansen,B.
  TITLE     Treatment of melanoma by reduction in clusterin levels
  JOURNAL   Patent: WO 2004018675-A 4 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 9
CQ786639/c
LOCUS       CQ786639                  21 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 28 from Patent WO2004018675.
ACCESSION   CQ786639
VERSION     CQ786639.1  GI:45721659
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jansen,B.
  TITLE     Treatment of melanoma by reduction in clusterin levels
  JOURNAL   Patent: WO 2004018675-A 28 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 10
CQ786178/c
LOCUS       CQ786178                  23 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 66 from Patent WO2004018676.
ACCESSION   CQ786178
VERSION     CQ786178.1  GI:45721281
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
  TITLE     Rnai probes targeting cancer-related proteins
  JOURNAL   Patent: WO 2004018676-A 66 04-MAR-2004;
            The University of British Columbia (CA)
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         21 GCAGCAGAGTCTTCATCAT 3


RESULT 11
AR302789/c
LOCUS       AR302789                 181 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 19 from patent US 6541603.
ACCESSION   AR302789
VERSION     AR302789.1  GI:31691276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 181)
  AUTHORS   Kirschling,D.J., Gudkov,A. and Roninson,I.B.
  TITLE     Genes and genetic elements associated with sensitivity to
            platinum-based drugs
  JOURNAL   Patent: US 6541603-A 19 01-APR-2003;
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ORIGIN

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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         71 GCAGCAGAGTCTTCATCAT 53


RESULT 12
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LOCUS       AR302784                  195 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 14 from patent US 6541603.
ACCESSION   AR302784
VERSION     AR302784.1  GI:31691271
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 195)
  AUTHORS   Kirschling,D.J., Gudkov,A. and Roninson,I.B.
  TITLE     Genes and genetic elements associated with sensitivity to
            platinum-based drugs
  JOURNAL   Patent: US 6541603-A 14 01-APR-2003;
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         85 GCAGCAGAGTCTTCATCAT 67


RESULT 13
CQ693037/c
LOCUS       CQ693037                  255 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 37963 from Patent WO02070737.
ACCESSION   CQ693037
VERSION     CQ693037.1  GI:42234544
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE     Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 37963 12-SEP-2002;
            Chondrogene Inc. (CA)
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
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Db         95 GCAGCAGAGTCTTCATCAT 77


RESULT 14
CQ688092/c
LOCUS       CQ688092                  270 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 33018 from Patent WO02070737.
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VERSION     CQ688092.1  GI:42219840
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE     Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 33018 12-SEP-2002;
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Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         60 GCAGCAGAGTCTTCATCAT 42


RESULT 15
AX895152/c
LOCUS       AX895152                  275 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 11015 from Patent EP1033401.
ACCESSION   AX895152
VERSION     AX895152.1  GI:40050036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 11015 06-SEP-2000;
            Genset (FR)
FEATURES             Location/Qualifiers
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ORIGIN

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Db        126 GCAGCAGAGTCTTCATCAT 108
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Job time : 1718 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 23:16:37 ; Search time 341 Seconds
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Title: US-10-646-436-10
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SUMMARIES

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	4	19	90.5	19	17	US-10-646-391A-43	Sequence 43, Appl
c	5	19	90.5	19	17	US-10-646-436-67	Sequence 67, Appl
	6	19	90.5	19	17	US-10-646-436-68	Sequence 68, Appl
	7	19	90.5	21	9	US-09-944-326-4	Sequence 4, Appli
	8	19	90.5	21	10	US-09-967-726A-4	Sequence 4, Appli
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c	19	19	90.5	255	17	US-10-085-783A-37963	Sequence 37963, A
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c	25	19	90.5	396	9	US-09-825-294-15	Sequence 15, Appl
c	26	19	90.5	396	9	US-09-970-966-15	Sequence 15, Appl
c	27	19	90.5	396	15	US-10-212-677-15	Sequence 15, Appl
c	28	19	90.5	396	17	US-10-361-811-15	Sequence 15, Appl
c	29	19	90.5	396	17	US-10-369-186-15	Sequence 15, Appl
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c	34	19	90.5	491	10	US-09-918-995-17455	Sequence 17455, A
c	35	19	90.5	492	10	US-09-918-995-31156	Sequence 31156, A
c	36	19	90.5	704	17	US-10-264-049-1985	Sequence 1985, Ap
c	37	19	90.5	1067	19	US-10-491-213-91	Sequence 91, Appl
c	38	19	90.5	1117	19	US-10-491-213-93	Sequence 93, Appl
c	39	19	90.5	1315	19	US-10-491-213-101	Sequence 101, App
c	40	19	90.5	1369	19	US-10-491-213-90	Sequence 90, Appl
c	41	19	90.5	1373	19	US-10-491-213-102	Sequence 102, App
c	42	19	90.5	1451	16	US-10-133-013-214	Sequence 214, App
c	43	19	90.5	1568	17	US-10-291-172-29	Sequence 29, Appl
c	44	19	90.5	1568	17	US-10-221-278-29	Sequence 29, Appl
c	45	19	90.5	1610	19	US-10-491-213-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-10-646-391A-29
; Sequence 29, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-29

Query Match 100.0%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9;
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RESULT 2
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; Publication No. US20040096882A1
; GENERAL INFORMATION:
;  APPLICANT: Jansen, Burkhard
;  APPLICANT:  Gleave, Martin
;  APPLICANT:  Signaevsky, Maxim
;  APPLICANT:  Beraldi, Eliana
;  APPLICANT:  Trougakos, Ioannis
;  APPLICANT:  Gonos, Efstathios
;  TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
;  FILE REFERENCE: UBC.P-030
;  CURRENT APPLICATION NUMBER: US/10/646,436
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-10

  Query Match             100.0%;  Score 21;  DB 17;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAUTT 21
                ||||||||||||||||||||
Db          1 GCAGCAGAGUCUUCAUCAUTT 21


RESULT 3
US-10-646-391A-42/c
; Sequence 42, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Jansen, Burkhard
;  TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
;  FILE REFERENCE: UBC.P-035
;  CURRENT APPLICATION NUMBER: US/10/646,391A
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/319,748
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-42

  Query Match             90.5%;  Score 19;  DB 17;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 26;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
                |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 4
US-10-646-391A-43
; Sequence 43, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Jansen, Burkhard
;  TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
;  FILE REFERENCE: UBC.P-035
;  CURRENT APPLICATION NUMBER: US/10/646,391A
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/319,748
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: RNAi fo rhuman clusterin
US-10-646-391A-43

  Query Match             90.5%;  Score 19;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
                |||||||||||||||||||
Db          1 GCAGCAGAGUCUUCAUCAU 19


RESULT 5
US-10-646-436-67/c
; Sequence 67, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
;  APPLICANT: Jansen, Burkhard
;  APPLICANT:  Gleave, Martin
;  APPLICANT:  Signaevsky, Maxim
;  APPLICANT:  Beraldi, Eliana
;  APPLICANT:  Trougakos, Ioannis
;  APPLICANT:  Gonos, Efstathios
;  TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
;  FILE REFERENCE: UBC.P-030
;  CURRENT APPLICATION NUMBER: US/10/646,436
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
;   LENGTH: 19
;   TYPE: RNA
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; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-67

Query Match 90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 73.7%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||||:|::||:||:
Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 6
US-10-646-436-68
; Sequence 68, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 19
; TYPE: RNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi fo rhuman clusterin
US-10-646-436-68

Query Match 90.5%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
|||||||||||||||||||
Db 1 GCAGCAGAGUCUUCAUCAU 19

RESULT 7
US-09-944-326-4
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4

Query Match 90.5%; Score 19; DB 9; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 8
US-09-967-726A-4
; Sequence 4, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-4

Query Match 90.5%; Score 19; DB 10; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 9
US-10-080-794-4
; Sequence 4, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

  Query Match             90.5%;  Score 19;  DB 16;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 27;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 10
US-10-646-391A-4
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Jansen, Burkhard
;  TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
;  FILE REFERENCE: UBC.P-035
;  CURRENT APPLICATION NUMBER: US/10/646,391A
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/319,748
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: human
US-10-646-391A-4

  Query Match             90.5%;  Score 19;  DB 17;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 27;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db          3 GCAGCAGAGTCTTCATCAT 21


RESULT 11
US-10-646-391A-28/c
; Sequence 28, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Jansen, Burkhard
;  TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
;  FILE REFERENCE: UBC.P-035
;  CURRENT APPLICATION NUMBER: US/10/646,391A
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/319,748
;  PRIOR FILING DATE: 2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-28

  Query Match             90.5%;  Score 19;  DB 17;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 27;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 12
US-10-646-436-9/c
; Sequence 9, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
;  APPLICANT: Jansen, Burkhard
;  APPLICANT:  Gleave, Martin
;  APPLICANT:  Signaevsky, Maxim
;  APPLICANT:  Beraldi, Eliana
;  APPLICANT:  Trougakos, Ioannis
;  APPLICANT:  Gonos, Efstathios
;  TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
;  FILE REFERENCE: UBC.P-030
;  CURRENT APPLICATION NUMBER: US/10/646,436
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: US 60/405,193
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/408,152
;  PRIOR FILING DATE: 2002-09-03
;  PRIOR APPLICATION NUMBER: US 60/473,387
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-9

  Query Match             90.5%;  Score 19;  DB 17;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 27;
  Matches   14;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAGCAGAGUCUUCAUCAU 19
              |||||||||:|::||:||:
Db         19 GCAGCAGAGTCTTCATCAT 1


RESULT 13
US-10-828-394-5
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
;  APPLICANT: Jackson, John
;  APPLICANT:  Burt, Helen
;  APPLICANT:  Springate, Christopher
;  APPLICANT:  Gleave, Martin
;  TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
;  FILE REFERENCE: UBC.P-033
;  CURRENT APPLICATION NUMBER: US/10/828,394
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 60/464,159
;  PRIOR FILING DATE: 2003-04-18
;  NUMBER OF SEQ ID NOS: 23
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

Query Match 90.5%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 14
US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-5

Query Match 90.5%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 3 GCAGCAGAGTCTTCATCAT 21

RESULT 15
US-10-646-436-66/c
; Sequence 66, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-10-646-436-66

Query Match 90.5%; Score 19; DB 17; Length 23;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCAGAGUCUUCAUCAU 19
||||||||:|::||:||:
Db 21 GCAGCAGAGTCTTCATCAT 3

Search completed: May 24, 2005, 00:29:27
Job time : 343 secs